IN THE CLAIMS:

Please cancel claims 52-69 without prejudice, add new claims 70-87, and amend the claims as follows:

1-33. (Canceled)

34. (Currently Amended) A method for delaying, repressing or otherwise reducing the expression of a target gene in an animal cell comprising introducing an RNA nucleic acid molecule to the cell, wherein the RNA nucleic acid molecule includes a transcription product of a genetic construct comprising a mammalian terminator and at least two copies of a structural gene sequence, wherein said structural gene sequence comprises a nucleotide sequence which is at least 80% identical to at least a region of said target gene, wherein at least one copy of said structural gene sequence is placed operably in the sense orientation and wherein at least one other copy of said structural gene sequence is placed operably in the antisense orientation.

35. (Previously Presented) The method of claim 34 wherein said at least two copies are operably under the control of a single promoter.

36. (Currently Amended) The method of claim 34 wherein said at least one copy is operably under the control of a first promoter and said at least one other copy is operably under the control of a second promoter.

37. (Previously Presented) The method according to claim 34, wherein said RNA nucleic acid molecule consists essentially of ribonucleotides.

38. (Previously Presented) The method according to claim 34, wherein said RNA nucleic acid molecule is comprised at least partially of ribonucleotide analogues.

39. (Previously Presented) The method according to claim 34, wherein said

structural gene sequence is about 20-30 nucleotides in length.

40. (Previously Presented) The method according to claim 34, wherein said structural gene sequence is 23 nucleotides in length.

41. (Previously Presented) The method according to claim 34, wherein said structural gene sequence is 22 nucleotides in length.

42. (Previously Presented) The method according to claim 34, wherein said structural gene sequence is 21 nucleotides in length.

43. (Previously Presented) The method according to claim 34, wherein said structural gene sequence is 20 nucleotides in length.

44. (Previously Presented) The method according to claim 34, wherein said structural gene sequence is 19 nucleotides in length.

45. (Previously Presented) The method according to claim 34, wherein said structural gene sequence is 18 nucleotides in length.

46. (Previously Presented) The method according to any one of claims 39-45, wherein said at least two copies are about the same length.

47. (Previously Presented) The method according to any one of claims 39-45, wherein said at least two copies are the same length.

48. (Previously Presented) The method according to claim 34, wherein said at least two copies are in the same nucleic acid strand.

49. (Previously Presented) The method according to claim 48, wherein said at least two copies are separated by at least one nucleic acid stuffer sequence.

50. (Previously Presented) The method according to claim 34, wherein said at least two copies are in separate nucleic acid strands.

51. (Previously Presented) The method according to claim 34, wherein said first RNA sequence is identical to the region of said target gene and second RNA sequence is identical to the complement of said region of said target gene.

52-69. (Canceled)

70. (New) A method for delaying, repressing or otherwise reducing the expression of a target gene in an animal cell comprising introducing an RNA nucleic acid molecule to the cell, wherein the RNA nucleic acid molecule includes a transcription product of a genetic construct comprising an avian terminator and at least two copies of a structural gene sequence, wherein said structural gene sequence comprises a nucleotide sequence which is at least 80% identical to at least a region of said target gene, wherein at least one copy of said structural gene sequence is placed operably in the sense orientation and wherein at least one other copy of said structural gene sequence is placed operably in the antisense orientation.

71. (New) The method of claim 70 wherein said at least two copies are operably under the control of a single promoter.

72. (New) The method of claim 70 wherein said at least one copy is operably under the control of a first promoter and said at least one other copy is operably under the control of a second promoter.

73. (New) The method according to claim 70, wherein said RNA nucleic acid molecule consists essentially of ribonucleotides.

74. (New) The method according to claim 70, wherein said RNA nucleic acid

molecule is comprised at least partially of ribonucleotide analogues.

75. (New) The method according to claim 70, wherein said structural gene sequence is about 20-30 nucleotides in length.

76. (New) The method according to claim 70, wherein said structural gene sequence is 23 nucleotides in length.

77. (New) The method according to claim 70, wherein said structural gene sequence is 22 nucleotides in length.

78. (New) The method according to claim 70, wherein said structural gene sequence is 21 nucleotides in length.

79. (New) The method according to claim 70, wherein said structural gene sequence is 20 nucleotides in length.

80. (New) The method according to claim 70, wherein said structural gene sequence is 19 nucleotides in length.

81. (New) The method according to claim 70, wherein said structural gene sequence is 18 nucleotides in length.

82. (New) The method according to any one of claims 75-81, wherein said at least two copies are about the same length.

83. (New) The method according to any one of claims 75-81, wherein said at least two copies are the same length.

84. (New) The method according to claim 70, wherein said at least two copies are in the same nucleic acid strand.

85. (New) The method according to claim 84, wherein said at least two copies are separated by at least one nucleic acid stuffer sequence.

86. (New) The method according to claim 70, wherein said at least two copies are in separate nucleic acid strands.

87. (New) The method according to claim 70, wherein said first RNA sequence is identical to the region of said target gene and second RNA sequence is identical to the complement of said region of said target gene.